



SEQUENCE LISTING

<110> Meyers, Rachel
Cook, William James
Williamson, Mark
Rudolph-Owen, Laura A.
Gimeno, Ruth

<120> 21481, A NOVEL DEHYDROGENASE MOLECULE
AND USES THEREFOR

<130> MPI00-079P1RCP2CN1M

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<141> 2003-09-17

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<151> 2001-04-18

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<151> 2001-03-23

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Trp Leu Asp Thr Gln Asp Arg Cys Leu Gly His Tyr Val Asn Gly Lys
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Trp Leu Lys Pro Glu His Arg Asn Ser Val Pro Cys Gln Asp Pro Ile
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Thr Gly Glu Asn Leu Ala Ser Cys Leu Gln Ala Gln Ala Glu Asp Val	
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gct gca gcc gtg qag gca gcc agg atg gca ttt aag ggc tgg agt qcg	347
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His Pro Gly Val Val Arg Ala Gln His Leu Thr Arg Leu Ala Glu Val	
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Ile Gln Lys His Gln Arg Leu Leu Trp Thr Leu Glu Ser Leu Val Thr	
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Gly Arg Ala Val Arg Glu Val Arg Asp Gly Asp Val Gln Leu Ala Gln	
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Gln Leu Leu His Tyr His Ala Ile Gln Ala Ser Thr Gln Glu Glu Ala	
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Thr Phe Ser Phe Leu Glu Met Met Trp Arg Ile Cys Pro Ala Leu Ala	
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Val Gly Cys Thr Val Val Ala Leu Val Pro Pro Ala Ser Pro Ala Pro	
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ctc ctc ctg gcc cag ctg gcg ggg gag ctg ggc ccc ttc ccg gga atc	731
Leu Leu Leu Ala Gln Leu Ala Gly Glu Leu Gly Pro Phe Pro Gly Ile	
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Leu Asn Val Val Ser Gly Pro Ala Ser Leu Val Pro Ile Leu Ala Ser	
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Gln Pro Gly Ile Arg Lys Val Ala Phe Cys Gly Ala Pro Glu Glu Gly	
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Arg Ala Leu Arg Arg Ser Leu Ala Gly Glu Cys Ala Glu Leu Gly Leu	
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Asp Ser Ala Val Glu Gly Val Val Asp Ala Ala Trp Ser Asp Arg Gly	
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ctg gat ggg gcc gtc gac atg ggg gcc cgg ggg gct gcc qca tgt qac Leu Asp Gly Ala Val Asp Met Gly Ala Arg Gly Ala Ala Ala Cys Asp 340 345 350	1115
ctg gtc cag cgc ttt gtg cgt gag gcc cag agc cag ggt gca cag gtg Leu Val Gln Arg Phe Val Arg Glu Ala Gln Ser Gln Gly Ala Gln Val 355 360 365	1163
ttc cag gct ggt gat gtg cct tcg gaa cgc cca ttc tat ccc cca acc Phe Gln Ala Gly Asp Val Pro Ser Glu Arg Pro Phe Tyr Pro Pro Thr 370 375 380	1211
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ccg tgg cct gtg gtc gtg gcc tcc ccc ttc cgc aca gcc aag gag gca Pro Trp Pro Val Val Ala Ser Pro Phe Arg Thr Ala Lys Glu Ala 400 405 410 415	1307
ctg ttg gtg gcc aac ggg acg ccc cgc ggg ggc agc gcc agt gtg tgg Leu Leu Val Ala Asn Gly Thr Pro Arg Gly Ser Ala Ser Val Trp 420 425 430	1355
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tca acc ctg ccg gct ggg cct gaa ata ggg ccc agc cca gca ccc ccc Ser Thr Leu Pro Ala Gly Pro Glu Ile Gly Pro Ser Pro Ala Pro Pro 515 520 525	1643
tat ggg ctc ttc gtt ggg ggc cgt ttc cag gct cct ggg gcc cga agc Tyr Gly Leu Phe Val Gly Arg Phe Gln Ala Pro Gly Ala Arg Ser 530 535 540	1691
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gcc caa ggc cac acc ctg cag gta gcc ggg ctg aga ggc cct gtg ctg Ala Gln Gly His Thr Leu Gln Val Ala Gly Leu Arg Gly Pro Val Leu 640 645 650 655	2027
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agc agg ggc tgc ccg cgg gcc tgg gac cag gag gcc gag ggg gca ggc Ser Arg Gly Cys Pro Arg Ala Trp Asp Gln Glu Ala Glu Gly Ala Gly 770 775 780	2411
cca gag ctg ggg ctg cga gtg gcg cgg acc aag gcc ctg tgg ctg cct Pro Glu Leu Gly Leu Arg Val Ala Arg Thr Lys Ala Leu Trp Leu Pro 785 790 795	2459
atg ggg gac tgatgcctga gcgccaccta ctgcattttg gacacacctac Met Gly Asp 800	2508
accaaggggga gatgcacccc acagacacct gggactttcc ccttctgggtt cctgtgtctc ccaataaaact ctctgaccaa ccctaaaaaa aaaaaaaaaa aaaaaaaaaa rwarmaactt ctggcagata tgaggcttt ttctttttt tt	2568 2628 2660

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35 40 45
Leu Lys Pro Glu His Arg Asn Ser Val Pro Cys Gln Asp Pro Ile Thr
50 55 60
Gly Glu Asn Leu Ala Ser Cys Leu Gln Ala Gln Ala Glu Asp Val Ala
65 70 75 80
Ala Ala Val Glu Ala Ala Arg Met Ala Phe Lys Gly Trp Ser Ala His
85 90 95
Pro Gly Val Val Arg Ala Gln His Leu Thr Arg Leu Ala Glu Val Ile
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Gln Lys His Gln Arg Leu Leu Trp Thr Leu Glu Ser Leu Val Thr Gly
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Arg Ala Val Arg Glu Val Arg Asp Gly Asp Val Gln Leu Ala Gln Gln
130 135 140
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Ala Gly Trp Glu Pro Met Gly Val Ile Gly Leu Ile Leu Pro Pro Thr
165 170 175
Phe Ser Phe Leu Glu Met Met Trp Arg Ile Cys Pro Ala Leu Ala Val
180 185 190
Gly Cys Thr Val Val Ala Leu Val Pro Pro Ala Ser Pro Ala Pro Leu
195 200 205
Leu Leu Ala Gln Leu Ala Gly Glu Leu Gly Pro Phe Pro Gly Ile Leu
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Asn Val Val Ser Gly Pro Ala Ser Leu Val Pro Ile Leu Ala Ser Gln
225 230 235 240
Pro Gly Ile Arg Lys Val Ala Phe Cys Gly Ala Pro Glu Glu Gly Arg
245 250 255
Ala Leu Arg Arg Ser Leu Ala Gly Glu Cys Ala Glu Leu Gly Leu Ala
260 265 270
Leu Gly Thr Glu Ser Leu Leu Leu Leu Thr Asp Thr Ala Asp Val Asp
275 280 285
Ser Ala Val Glu Gly Val Val Asp Ala Ala Trp Ser Asp Arg Gly Pro
290 295 300
Gly Gly Leu Arg Leu Leu Ile Gln Glu Ser Val Trp Asp Glu Ala Met
305 310 315 320
Arg Arg Leu Gln Glu Arg Met Gly Arg Leu Arg Ser Gly Arg Gly Leu
325 330 335
Asp Gly Ala Val Asp Met Gly Ala Arg Gly Ala Ala Ala Cys Asp Leu
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Val Gln Arg Phe Val Arg Glu Ala Gln Ser Gln Gly Ala Gln Val Phe
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Gln Ala Gly Asp Val Pro Ser Glu Arg Pro Phe Tyr Pro Pro Thr Leu
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Val Ser Asn Leu Pro Pro Ala Ser Pro Cys Ala Gln Val Glu Val Pro
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Trp Pro Val Val Val Ala Ser Pro Phe Arg Thr Ala Lys Glu Ala Leu
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Gly	Leu	Phe	Val	Gly	Gly	Arg	Phe	Gln	Ala	Pro	Gly	Ala	Arg	Ser	Ser
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Arg	Pro	Ile	Arg	Asp	Ser	Ser	Gly	Asn	Leu	His	Gly	Tyr	Val	Ala	Glu
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Phe	Pro	Gly	Trp	Ala	Gly	Gln	Ser	Pro	Gly	Ala	Arg	Ala	Ala	Leu	Leu
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Trp	Ala	Leu	Ala	Ala	Leu	Glu	Arg	Arg	Lys	Ser	Thr	Leu	Ala	Ser	
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Arg	Leu	Glu	Arg	Gln	Gly	Ala	Glu	Leu	Lys	Ala	Ala	Glu	Ala	Glu	Val
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Gln	Gly	His	Thr	Leu	Gln	Val	Ala	Gly	Leu	Arg	Gly	Pro	Val	Leu	Arg
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Leu	Arg	Glu	Pro	Leu	Gly	Val	Leu	Ala	Val	Val	Cys	Pro	Asp	Glu	Trp
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Pro	Leu	Leu	Ala	Phe	Val	Ser	Leu	Leu	Ala	Pro	Ala	Leu	Ala	Tyr	Gly
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Asn	Thr	Val	Val	Met	Val	Pro	Ser	Ala	Ala	Cys	Pro	Leu	Leu	Ala	Leu
				690				695				700			
Glu	Val	Cys	Gln	Asp	Met	Ala	Thr	Val	Phe	Pro	Ala	Gly	Leu	Ala	Asn
705					710					715					720
Val	Val	Thr	Gly	Asp	Arg	Asp	His	Leu	Thr	Arg	Cys	Leu	Ala	Leu	His
					725				730				735		
Gln	Asp	Val	Gln	Ala	Met	Trp	Tyr	Phe	Gly	Ser	Ala	Gln	Gly	Ser	Gln
					740				745				750		
Phe	Val	Glu	Trp	Ala	Ser	Ala	Gly	Asn	Leu	Lys	Pro	Val	Trp	Ala	Ser
				755				760				765			
Arg	Gly	Cys	Pro	Arg	Ala	Trp	Asp	Gln	Glu	Ala	Glu	Gly	Ala	Gly	Pro
770					775					780					
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Leu Glu Tyr Gly Pro Val Pro Glu Ser His Ala Cys Ala Leu Ala Trp
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Leu Lys Pro Glu His Arg Asn Ser Val Pro Cys Gln Asp Pro Ile Thr			
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gga gag aac ttg gcc agt tgc ctg cag gca cag gcc gag gat gtg gct	240		
Gly Glu Asn Leu Ala Ser Cys Leu Gln Ala Gln Ala Glu Asp Val Ala			
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gca gcc gtg gag gca gcc agg atg gca ttt aag ggc tgg agt gcg cac	288		
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85	90	95	
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Pro Gly Val Val Arg Ala Gln His Leu Thr Arg Leu Ala Glu Val Ile			
100	105	110	
cag aag cac cag cgg ctg ctg tgg acc ctg gaa tcc ctg gtg act ggg	384		
Gln Lys His Gln Arg Leu Leu Trp Thr Leu Glu Ser Leu Val Thr Gly			
115	120	125	
cgg gct gtt cga gag gtt cga gac ggg gac gtc cag ctg gcc cag cag	432		
Arg Ala Val Arg Glu Val Arg Asp Gly Asp Val Gln Leu Ala Gln Gln			
130	135	140	
ctg ctc cac tac cat gca atc cag gca tcc acc cag gag gag gca ctg	480		
Leu Leu His Tyr His Ala Ile Gln Ala Ser Thr Gln Glu Glu Ala Leu			
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gca ggc tgg gag ccc atg gga gta att ggc ctc atc ctg cca ccc aca	528		
Ala Gly Trp Glu Pro Met Gly Val Ile Gly Leu Ile Leu Pro Pro Thr			
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Phe Ser Phe Leu Glu Met Met Trp Arg Ile Cys Pro Ala Leu Ala Val			
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Gly Cys Thr Val Val Ala Leu Val Pro Pro Ala Ser Pro Ala Pro Leu			
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Leu Leu Ala Gln Leu Ala Gly Glu Leu Gly Pro Phe Pro Gly Ile Leu			
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325 330 335	
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cag gct ggt gat gtg cct tcg gaa cgc cca ttc tat ccc cca acc ttg Gln Ala Gly Asp Val Pro Ser Glu Arg Pro Phe Tyr Pro Pro Thr Leu	1152
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Trp Ala Leu Ala Ala Leu Glu Arg Arg Lys Ser Thr Leu Ala Ser	
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Arg Leu Glu Arg Gln Gly Ala Glu Leu Lys Ala Ala Glu Ala Glu Val	
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Glu Leu Ser Ala Arg Arg Leu Arg Ala Trp Gly Ala Arg Val Gln Ala	
625 630 635 640	
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Gln Gly His Thr Leu Gln Val Ala Gly Leu Arg Gly Pro Val Leu Arg	
645 650 655	
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aac act gtg gtc atg gtg ccc agt gcg gcc tgt cct ctg ctg gcc ctg	2112
Asn Thr Val Val Met Val Pro Ser Ala Ala Cys Pro Leu Leu Ala Leu	
690 695 700	
gag gtc tgc cag gac atg gcc acc gtg ttc cca gca ggc ctg gcc aac	2160
Glu Val Cys Gln Asp Met Ala Thr Val Phe Pro Ala Gly Leu Ala Asn	
705 710 715 720	
gtg gtg aca gga gac cgg gac cat ctg acc cg ^c tgc ctg gcc ttg cac	2208
Val Val Thr Gly Asp Arg Asp His Leu Thr Arg Cys Leu Ala Leu His	
725 730 735	
caa gac gtc cag gcc atg tgg tat ttc gga tca gcc cag ggt tcc cag	2256
Gln Asp Val Gln Ala Met Trp Tyr Phe Gly Ser Ala Gln Gly Ser Gln	
740 745 750	
ttt gtc gag tgg gcc tcg gca gga aac ctc aaa cc ^g gtg tgg gcg agc	2304
Phe Val Glu Trp Ala Ser Ala Gly Asn Leu Lys Pro Val Trp Ala Ser	
755 760 765	
agg ggc tgc cc ^g cgg gcc tgg gac cag gag gcc gag ggg gca ggc cca	2352
Arg Gly Cys Pro Arg Ala Trp Asp Gln Glu Ala Glu Gly Ala Gly Pro	
770 775 780	
gag ctg ggg ctg cga gtg gcg cg ^g acc aag gcc ctg tgg ctg cct atg	2400
Glu Leu Gly Leu Arg Val Ala Arg Thr Lys Ala Leu Trp Leu Pro Met	
785 790 795 800	

ggg gac
Gly Asp

2406

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cccctggatt cggctcgctt tcggagacac tgtgagtaac ttccttattt ttaaacattt 180
ggggatttagc acgcccactg ggtttcagc ttggaggctt gcacagagct gagctccctg 240
cagccttggg cctccccctg ccctgggagt cctgatcagc gtcttttgc aaagccaatc 300
cccttttact ccgttgtccc ccagaacaag atg gga gtc atg gcc atg ctg atg 354
Met Gly Val Met Ala Met Leu Met
1 5

ctc ccc ctg ctg ctg gga atc agc ggc ctc ctc ttc att tac caa 402
Leu Pro Leu Leu Leu Leu Gly Ile Ser Gly Leu Leu Phe Ile Tyr Gln
10 15 20

gag gtg tcc agg ctg tgg tca aag tca gct gtg cag aac aaa gtg gtg 450
Glu Val Ser Arg Leu Trp Ser Lys Ser Ala Val Gln Asn Lys Val Val
25 30 35 40

gtg atc acc gat gcc atc tca gga ctg ggc aag gag tgt gct cgg gtg 498
Val Ile Thr Asp Ala Ile Ser Gly Leu Gly Lys Glu Cys Ala Arg Val
45 50 55

ttc cac aca ggt ggg gca agg ctg gtg ctg tgt gga aag aac tgg gag 546
Phe His Thr Gly Gly Ala Arg Leu Val Leu Cys Gly Lys Asn Trp Glu
60 65 70

agg cta gag aac cta tat gat gcc ttg atc agc gtg gct gac ccc agc 594
Arg Leu Glu Asn Leu Tyr Asp Ala Leu Ile Ser Val Ala Asp Pro Ser
75 80 85

aag aca ttc acc cca aag ctg gtc ctg ttg gac ctc tca gac atc agc 642
Lys Thr Phe Thr Pro Lys Leu Val Leu Asp Leu Ser Asp Ile Ser
90 95 100

tgt gtc cca gat gtg gca aaa gaa gtc ctg gat tgc tat ggc tgt gtg 690
Cys Val Pro Asp Val Ala Lys Glu Val Leu Asp Cys Tyr Gly Cys Val
105 110 115 120

gac atc ctc atc aac aat gcc agt gtg aag gtg aag ggg cct gcc cat 738
Asp Ile Leu Ile Asn Asn Ala Ser Val Lys Val Lys Gly Pro Ala His
125 130 135

aag att tct ctg gag ctc gac aaa aag atc atg gat gcc aat tac ttt 786
Lys Ile Ser Leu Glu Leu Asp Lys Lys Ile Met Asp Ala Asn Tyr Phe
140 145 150

ggc ccc atc aca ttg acg aaa gcc ctg ctt ccc aac atg atc tcc cg	834
Gly Pro Ile Thr Leu Thr Lys Ala Leu Leu Pro Asn Met Ile Ser Arg	
155 160 165	
aga aca ggc caa atc gtg tta gtg aat aat atc caa ggg aag ttt gga	882
Arg Thr Gly Gln Ile Val Leu Val Asn Asn Ile Gln Gly Lys Phe Gly	
170 175 180	
atc ccg ttc cgt acg act tac gct gcc tcc aag cac gca gcc ctg ggc	930
Ile Pro Phe Arg Thr Tyr Ala Ala Ser Lys His Ala Ala Leu Gly	
185 190 195 200	
ttc ttt gac tgc ctc cga gcc gaa gtg gag gaa tac gat gtt gtc atc	978
Phe Phe Asp Cys Leu Arg Ala Glu Val Glu Glu Tyr Asp Val Val Ile	
205 210 215	
agc acc gtg agc ccg act ttc atc cgg tcg tac cac gtg tat cca gag	1026
Ser Thr Val Ser Pro Thr Ile Arg Ser Tyr His Val Tyr Pro Glu	
220 225 230	
caa gga aac tgg gaa gct tcc att tgg aaa ttc ttt ttc agg aag ctg	1074
Gln Gly Asn Trp Glu Ala Ser Ile Trp Lys Phe Phe Arg Lys Leu	
235 240 245	
acc tac ggc gtg cac cca gta gag gtg gcg gag gag gtg atg cgc acc	1122
Thr Tyr Gly Val His Pro Val Glu Val Ala Glu Glu Val Met Arg Thr	
250 255 260	
gtg cgg agg aag aag caa gag gtg ttt atg gcc aac ccc atc ccc aag	1170
Val Arg Arg Lys Lys Gln Glu Val Phe Met Ala Asn Pro Ile Pro Lys	
265 270 275 280	
gcc gcc gtg tac gtc cgc acc ttc ttc ccg gag ttc ttt ttc gcc gtg	1218
Ala Ala Val Tyr Val Arg Thr Phe Phe Pro Glu Phe Phe Ala Val	
285 290 295	
gtg gcc tgt ggg gtg aag gag aag ctc aat gtc ccg gag gag ggg	1263
Val Ala Cys Gly Val Lys Glu Lys Leu Asn Val Pro Glu Glu Gly	
300 305 310	
taactgcagg aggccaaatg ggccacccct tggaaataaa ggttttctg gcaaaaaaaaaa	1323
aaaaaaaaaa aaanttgcg gccgcaagct tattccctt agggagggtt aatttt	1379
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Ser Ala Val Gln Asn Lys Val Val Ile Thr Asp Ala Ile Ser Gly	
35 40 45	
Leu Gly Lys Glu Cys Ala Arg Val Phe His Thr Gly Gly Ala Arg Leu	
50 55 60	
Val Leu Cys Gly Lys Asn Trp Glu Arg Leu Glu Asn Leu Tyr Asp Ala	
65 70 75 80	
Leu Ile Ser Val Ala Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val	
85 90 95	
Leu Leu Asp Leu Ser Asp Ile Ser Cys Val Pro Asp Val Ala Lys Glu	
100 105 110	

Val Leu Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser
 115 120 125
 Val Lys Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys
 130 135 140
 Lys Ile Met Asp Ala Asn Tyr Phe Gly Pro Ile Thr Leu Thr Lys Ala
 145 150 155 160
 Leu Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val
 165 170 175
 Asn Asn Ile Gln Gly Lys Phe Gly Ile Pro Phe Arg Thr Thr Tyr Ala
 180 185 190
 Ala Ser Lys His Ala Ala Leu Gly Phe Phe Asp Cys Leu Arg Ala Glu
 195 200 205
 Val Glu Glu Tyr Asp Val Val Ile Ser Thr Val Ser Pro Thr Phe Ile
 210 215 220
 Arg Ser Tyr His Val Tyr Pro Glu Gln Gly Asn Trp Glu Ala Ser Ile
 225 230 235 240
 Trp Lys Phe Phe Arg Lys Leu Thr Tyr Gly Val His Pro Val Glu
 245 250 255
 Val Ala Glu Glu Val Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val
 260 265 270
 Phe Met Ala Asn Pro Ile Pro Lys Ala Ala Val Tyr Val Arg Thr Phe
 275 280 285
 Phe Pro Glu Phe Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys
 290 295 300
 Leu Asn Val Pro Glu Glu Gly
 305 310

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 <213> Homo sapiens

<220>
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 agc ggc ctc ctc ttc att tac caa gag gtg tcc agg ctg tgg tca aag 96
 Ser Gly Leu Leu Phe Ile Tyr Gln Glu Val Ser Arg Leu Trp Ser Lys
 20 25 30
 tca gct gtg cag aac aaa gtg gtg atc acc gat gcc atc tca gga 144
 Ser Ala Val Gln Asn Lys Val Val Val Ile Thr Asp Ala Ile Ser Gly
 35 40 45
 ctg ggc aag gag tgt gct cgg gtg ttc cac aca ggt ggg gca agg ctg 192
 Leu Gly Lys Glu Cys Ala Arg Val Phe His Thr Gly Gly Ala Arg Leu
 50 55 60
 gtg ctg tgt gga aag aac tgg gag agg cta gag aac cta tat gat gcc 240
 Val Leu Cys Gly Lys Asn Trp Glu Arg Leu Glu Asn Leu Tyr Asp Ala
 65 70 75 80
 ttg atc agc gtg gct gac ccc agc aag aca ttc acc cca aag ctg gtc 288
 Leu Ile Ser Val Ala Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val
 85 90 95
 ctg ttg gac ctc tca gac atc agc tgt gtc cca gat gtg gca aaa gaa 336
 Leu Leu Asp Leu Ser Asp Ile Ser Cys Val Pro Asp Val Ala Lys Glu

100	105	110	
gtc ctg gat tgc tat ggc tgt gtg gac atc ctc atc aac aat gcc agt			384
Val Leu Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser			
115	120	125	
gtg aag gtg aag ggg cct gcc cat aag att tct ctg gag ctc gac aaa			432
Val Lys Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys			
130	135	140	
aag atc atg gat gcc aat tac ttt ggc ccc atc aca ttg acg aaa gcc			480
Lys Ile Met Asp Ala Asn Tyr Phe Gly Pro Ile Thr Leu Thr Lys Ala			
145	150	155	160
ctg ctt ccc aac atg atc tcc cgg aga aca ggc caa atc gtg tta gtg			528
Leu Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val			
165	170	175	
aat aat atc caa ggg aag ttt gga atc ccg ttc cgt acg act tac gct			576
Asn Asn Ile Gln Gly Lys Phe Gly Ile Pro Phe Arg Thr Thr Tyr Ala			
180	185	190	
gcc tcc aag cac gca gcc ctg ggc ttc ttt gac tgc ctc cga gcc gaa			624
Ala Ser Lys His Ala Ala Leu Gly Phe Phe Asp Cys Leu Arg Ala Glu			
195	200	205	
gtg gag gaa tac gat gtt gtc atc agc acc gtg agc ccg act ttc atc			672
Val Glu Glu Tyr Asp Val Val Ile Ser Thr Val Ser Pro Thr Phe Ile			
210	215	220	
cgg tcg tac cac gtg tat cca gag caa gga aac tgg gaa gct tcc att			720
Arg Ser Tyr His Val Tyr Pro Glu Gln Gly Asn Trp Glu Ala Ser Ile			
225	230	235	240
tgg aaa ttc ttt ttc agg aag ctg acc tac ggc gtg cac cca gta gag			768
Trp Lys Phe Phe Arg Lys Leu Thr Tyr Gly Val His Pro Val Glu			
245	250	255	
gtg gcg gag gag gtg atg cgc acc gtg cgg agg aag aag caa gag gtg			816
Val Ala Glu Glu Val Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val			
260	265	270	
ttt atg gcc aac ccc atc ccc aag gcc gtc gtg tac gtc cgc acc ttc			864
Phe Met Ala Asn Pro Ile Pro Lys Ala Ala Val Tyr Val Arg Thr Phe			
275	280	285	
ttc ccg gag ttc ttt ttc gcc gtg gtg gcc tgt ggg gtg aag gag aag			912
Phe Pro Glu Phe Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys			
290	295	300	
ctc aat gtc ccg gag gag ggg			933
Leu Asn Val Pro Glu Glu Gly			
305	310		

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<220>
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 gacggcaggt ggcctggttc ctgcagctcc caggatcagc tctgccctcc cccaaacgc 180
 cagcctcgtc accegctccag ggcacctcca gcagtaacag gtggttcagc cagttggcag 240
 ccagccctg gatgagccaa gtccttccc ccagccaggc atg gcc gac tct gca 295
 Met Ala Asp Ser Ala
 1 5

cag gcc cag aag ctg gtg tac ctg gtc aca ggg ggc tgt ggc ttc ctg 343
 Gln Ala Gln Lys Leu Val Tyr Leu Val Thr Gly Gly Cys Gly Phe Leu
 10 15 20

gga gag cac gtg gtg cga atg ctg ctg cag cgg gag ccc cgg ctc ggg 391
 Gly Glu His Val Val Arg Met Leu Leu Gln Arg Glu Pro Arg Leu Gly
 25 30 35

gag ctg cgg gtc ttt gac caa cac ctg ggt ccc tgg ctg gag gag ctg 439
 Glu Leu Arg Val Phe Asp Gln His Leu Gly Pro Trp Leu Glu Glu Leu
 40 45 50

aag aca ggg cct gtg agg gtg act gcc atc cag ggg gac gtg acc cag 487
 Lys Thr Gly Pro Val Arg Val Thr Ala Ile Gln Gly Asp Val Thr Gln
 55 60 65

gcc cat gag gtg gca gca gct gtg gcc gga gcc cat gtg gtc atc cac 535
 Ala His Glu Val Ala Ala Val Ala Gly Ala His Val Val Ile His
 70 75 80 85

acg gct ggg ctg gta gac gtg ttt ggc agg gcc agt ccc aag acc atc 583
 Thr Ala Gly Leu Val Asp Val Phe Gly Arg Ala Ser Pro Lys Thr Ile
 90 95 100

cat gag gtc aac gtg cag ggt acc cgg aac gtg atc gag gct tgt gtg 631
 His Glu Val Asn Val Gln Gly Thr Arg Asn Val Ile Glu Ala Cys Val
 105 110 115

cag acc gga aca cgg ttc ctg gtc tac acc agc agc atg gaa gtt gtg 679
 Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser Ser Met Glu Val Val
 120 125 130

ggg cct aac acc aaa ggt cac ccc ttc tac agg ggc aac gaa gac acc 727
 Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg Gly Asn Glu Asp Thr
 135 140 145

cca tac gaa gca gtg cac agg cac ccc tat cct tgc agc aag gcc ctg 775
 Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro Cys Ser Lys Ala Leu
 150 155 160 165

gcc gag tgg ctg gtc ctg gag gcc aac ggg agg aag gtc cgt ggg ggg 823
 Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg Lys Val Arg Gly Gly
 170 175 180

ctg ccc ctg gtg acg tgt gcc ctt cgt ccc acg ggc atc tac ggt gaa 871
 Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr Gly Ile Tyr Gly Glu
 185 190 195

ggc cac cag atc atg agg gac ttc tac cgc cag ggc ctg cgc ctg gga 919
 Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln Gly Leu Arg Leu Gly
 200 205 210

ggt tgg ctc ttc cgg gcc atc ccg gcc tct gtg gag cat ggc cgg gtc	967
Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val Glu His Gly Arg Val	
215 220 225	
tat gtg ggc aat gtt gcc tgg atg cac gtg ctg gca gcc cgg gag ctg	1015
Tyr Val Gly Asn Val Ala Trp Met His Val Leu Ala Ala Arg Glu Leu	
230 235 240 245	
gag cag cgg gca gcc ctg atg ggc ggc cag gta tac ttc tgc tac gat	1063
Glu Gln Arg Ala Ala Leu Met Gly Gly Gln Val Tyr Phe Cys Tyr Asp	
250 255 260	
gga tca ccc tac agg agc tac gag gat ttc aac atg gag ttc ctg ggc	1111
Gly Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn Met Glu Phe Leu Gly	
265 270 275	
ccc tgc gga ctg cgg ctg gtg ggc gcc cgc cca ttg ctg ccc tac tgg	1159
Pro Cys Gly Leu Arg Leu Val Gly Ala Arg Pro Leu Leu Pro Tyr Trp	
280 285 290	
ctg ctg gtg ttc ctg gct gcc ctc aat gcc ctg ctg cag tgg ctg ctg	1207
Leu Leu Val Phe Leu Ala Ala Leu Asn Ala Leu Leu Gln Trp Leu Leu	
295 300 305	
cgg cca ctg gtg ctc tac gca ccc ctg ctg aac ccc tac acg ctg gcc	1255
Arg Pro Leu Val Leu Tyr Ala Pro Leu Leu Asn Pro Tyr Thr Leu Ala	
310 315 320 325	
gtg gcc aac acc acc ttc acc gtc agc acc gac aag gct cag cgc cat	1303
Val Ala Asn Thr Thr Phe Thr Val Ser Thr Asp Lys Ala Gln Arg His	
330 335 340	
ttc ggc tat gag ccc ctg ttc tcg tgg gag gat agc cgg acc cgc acc	1351
Phe Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp Ser Arg Thr Arg Thr	
345 350 355	
att ctc tgg gta cag gcc gct acg ggt tca gcc cag tgacgggtggg	1397
Ile Leu Trp Val Gln Ala Ala Thr Gly Ser Ala Gln	
360 365	
gctggggccct ggaggcccag atacagcaca tccacccagg tcccggagccc tcacaccctg	1457
gacgggaagg gacagctgca ttccagagca ggaggcaggg ctctggggcc agaatggctg	1517
tccttgcgt agagccctcc acattttctt tttctttttt gagacaggggt cttgctctgt	1577
cacccagact ggaatgcaag tgggtgtgant cataagctca ctnngmacct yaanccttct	1637
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Glu Pro Arg Leu Gly Glu Leu Arg Val Phe Asp Gln His Leu Gly Pro	
35 40 45	
Trp Leu Glu Glu Leu Lys Thr Gly Pro Val Arg Val Thr Ala Ile Gln	
50 55 60	
Gly Asp Val Thr Gln Ala His Glu Val Ala Ala Val Ala Gly Ala	
65 70 75 80	

His Val Val Ile His Thr Ala Gly Leu Val Asp Val Phe Gly Arg Ala
 85 90 95
 Ser Pro Lys Thr Ile His Glu Val Asn Val Gln Gly Thr Arg Asn Val
 100 105 110
 Ile Glu Ala Cys Val Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser
 115 120 125
 Ser Met Glu Val Val Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg
 130 135 140
 Gly Asn Glu Asp Thr Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro
 145 150 155 160
 Cys Ser Lys Ala Leu Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg
 165 170 175
 Lys Val Arg Gly Gly Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr
 180 185 190
 Gly Ile Tyr Gly Glu Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln
 195 200 205
 Gly Leu Arg Leu Gly Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val
 210 215 220
 Glu His Gly Arg Val Tyr Val Gly Asn Val Ala Trp Met His Val Leu
 225 230 235 240
 Ala Ala Arg Glu Leu Glu Gln Arg Ala Ala Leu Met Gly Gly Gln Val
 245 250 255
 Tyr Phe Cys Tyr Asp Gly Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn
 260 265 270
 Met Glu Phe Leu Gly Pro Cys Gly Leu Arg Leu Val Gly Ala Arg Pro
 275 280 285
 Leu Leu Pro Tyr Trp Leu Leu Val Phe Leu Ala Ala Leu Asn Ala Leu
 290 295 300
 Leu Gln Trp Leu Leu Arg Pro Leu Val Leu Tyr Ala Pro Leu Leu Asn
 305 310 315 320
 Pro Tyr Thr Leu Ala Val Ala Asn Thr Thr Phe Thr Val Ser Thr Asp
 325 330 335
 Lys Ala Gln Arg His Phe Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp
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 Ser Arg Thr Arg Thr Ile Leu Trp Val Gln Ala Ala Thr Gly Ser Ala
 355 360 365
 Gln

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 <211> 1107
 <212> DNA
 <213> Homo sapiens

<220>
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 ggc tgt ggc ttc ctg gga gag cac gtg gtg cga atg ctg ctg cag cgg 96
 Gly Cys Gly Phe Leu Gly Glu His Val Val Arg Met Leu Leu Gln Arg
 20 25 30

 gag ccc cgg ctc ggg gag ctg cgg gtc ttt gac caa cac ctg ggt ccc 144
 Glu Pro Arg Leu Gly Glu Leu Arg Val Phe Asp Gln His Leu Gly Pro
 35 40 45

 tgg ctg gag gag ctg aag aca ggg cct gtg agg gtg act gcc atc cag 192
 Trp Leu Glu Glu Leu Lys Thr Gly Pro Val Arg Val Thr Ala Ile Gln

50	55	60	
ggg gac gtg acc cag gcc cat gag gtg gca gca gct gtg gcc gga gcc			240
Gly Asp Val Thr Gln Ala His Glu Val Ala Ala Ala Val Ala Gly Ala			
65 70 75 80			
cat gtg gtc atc cac acg gct ggg ctg gta gac gtg ttt ggc agg gcc			288
His Val Val Ile His Thr Ala Gly Leu Val Asp Val Phe Gly Arg Ala			
85 90 95			
agt ccc aag acc atc cat gag gtc aac gtg cag ggt acc cgg aac gtg			336
Ser Pro Lys Thr Ile His Glu Val Asn Val Gln Gly Thr Arg Asn Val			
100 105 110			
atc gag gct tgt gtg cag acc gga aca cgg ttc ctg gtc tac acc agc			384
Ile Glu Ala Cys Val Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser			
115 120 125			
agc atg gaa gtt gtg ggg cct aac acc aaa ggt cac ccc ttc tac agg			432
Ser Met Glu Val Val Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg			
130 135 140			
ggc aac gaa gac acc cca tac gaa gca gtg cac agg cac ccc tat cct			480
Gly Asn Glu Asp Thr Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro			
145 150 155 160			
tgc agc aag gcc ctg gcc gag tgg ctg gtc ctg gag gcc aac ggg agg			528
Cys Ser Lys Ala Leu Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg			
165 170 175			
aag gtc cgt ggg ggg ctg ccc ctg gtg acg tgt gcc ctt cgt ccc acg			576
Lys Val Arg Gly Gly Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr			
180 185 190			
ggc atc tac ggt gaa ggc cac cag atc atg agg gac ttc tac cgc cag			624
Gly Ile Tyr Gly Glu Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln			
195 200 205			
ggc ctg cgc ctg gga ggt tgg ctc ttc cgg gcc atc ccg gcc tct gtg			672
Gly Leu Arg Leu Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val			
210 215 220			
gag cat ggc cgg gtc tat gtg ggc aat gtt gcc tgg atg cac gtg ctg			720
Glu His Gly Arg Val Tyr Val Gly Asn Val Ala Trp Met His Val Leu			
225 230 235 240			
gca gcc cgg gag ctg gag cag cgg gca gcc ctg atg ggc ggc cag gta			768
Ala Ala Arg Glu Leu Glu Gln Arg Ala Ala Leu Met Gly Gly Gln Val			
245 250 255			
tac ttc tgc tac gat gga tca ccc tac agg agc tac gag gat ttc aac			816
Tyr Phe Cys Tyr Asp Gly Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn			
260 265 270			
atg gag ttc ctg ggc ccc tgc gga ctg cgg ctg gtg ggc gcc cgc cca			864
Met Glu Phe Leu Gly Pro Cys Gly Leu Arg Leu Val Gly Ala Arg Pro			
275 280 285			
ttg ctg ccc tac tgg ctg ctg gtg ttc ctg gct gcc ctc aat gcc ctg			912
Leu Leu Pro Tyr Trp Leu Leu Val Phe Leu Ala Ala Leu Asn Ala Leu			
290 295 300			
ctg cag tgg ctg ctg cgg cca ctg gtg ctc tac gca ccc ctg ctg aac			960
Leu Gln Trp Leu Leu Arg Pro Leu Val Leu Tyr Ala Pro Leu Leu Asn			

305	310	315	320	
ccc tac acg ctg gcc gtg gcc aac acc acc ttc acc gtc agc acc gac Pro Tyr Thr Leu Ala Val Ala Asn Thr Thr Phe Thr Val Ser Thr Asp				1008
325		330	335	
aag gct cag cgc cat ttc ggc tat gag ccc ctg ttc tcg tgg gag gat Lys Ala Gln Arg His Phe Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp				1056
340	345		350	
agc cgg acc cgc acc att ctc tgg gta cag gcc gct acg ggt tca gcc Ser Arg Thr Arg Thr Ile Leu Trp Val Gln Ala Ala Thr Gly Ser Ala				1104
355	360		365	
cag Gln				1107
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1	5	10	15	
gct gca ggg atg gcc tcc tgg gct aag ggc agg agc tac ctg gcg cct 156 Ala Ala Gly Met Ala Ser Trp Ala Lys Gly Arg Ser Tyr Leu Ala Pro				
20	25	30		
ggt ttg ctg cag ggc caa gtg gcc atc gtc acc ggc ggg gcc acg ggc 204 Gly Leu Leu Gln Gly Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly				
35	40	45		
atc gga aaa gcc atc gtg aag gag ctc ctg gag ctg ggg agt aat gtg 252 Ile Gly Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val				
50	55	60		
gtc att gca tcc cgt aag ttg gag aga ttg aag tct gcg gca gat gaa 300 Val Ile Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu				
65	70	75	80	
ctg cag gcc aac cta cct ccc aca aag cag gca cga gtc att ccc ata 348 Leu Gln Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile				
85	90	95		
caa tgc aac atc cgg aat gag gag gag gtg aat aat ttg gtc aaa tct 396 Gln Cys Asn Ile Arg Asn Glu Glu Val Asn Asn Leu Val Lys Ser				
100	105	110		
acc tta gat act ttt ggt aag atc aat ttc ttg gtg aac aat gga gga 444 Thr Leu Asp Thr Phe Gly Lys Ile Asn Phe Leu Val Asn Asn Gly Gly				
115	120	125		
ggc cag ttt ctt tcc cct gct gaa cac atc agt tct aag gga tgg cac 492 Gly Gln Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His				

130	135	140	
gct gtg ctt gag acc aac ctg acg ggt acc ttc tac atg tgc aaa gca Ala Val Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala 145 150 155 160			
gtt tac agc tcc tgg atg aaa gag cat gga gga tct atc gtc aat atc Val Tyr Ser Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile 165 170 175			
att gtc cct act aaa gct gga ttt cca tta gct gtg cat tct gga gct Ile Val Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala 180 185 190			
gca aga gca ggt gtt tac aac ctc acc aaa tct tta gct ttg gaa tgg Ala Arg Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp 195 200 205			
gcc tgc agt gga ata cgg atc aat tgt gtt gcc cct gga gtt att tat Ala Cys Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr 210 215 220			
tcc cag act gct gtg gag aac tat ggt tcc tgg gga caa agc ttc ttt Ser Gln Thr Ala Val Glu Asn Tyr Gly Ser Trp Gly Gln Ser Phe Phe 225 230 235 240			
gaa ggg tct ttt cag aaa atc ccc gct aaa cga att ggt gtt cct gag Glu Gly Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu 245 250 255			
gag gtc tcc tct gtg gtc ttc cta ctg tct cct gca gct tcc ttc Glu Val Ser Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe 260 265 270			
atc act gga cag tcg gtg gat gtg gat ggg ggc cgg agt ctc tat act Ile Thr Gly Gln Ser Val Asp Val Asp Gly Gly Arg Ser Leu Tyr Thr 275 280 285			
cac tcg tat gag gta cca gat cat gac aac tgg ccc aag gga gca ggg His Ser Tyr Glu Val Pro Asp His Asp Asn Trp Pro Lys Gly Ala Gly 290 295 300			
gac ctt tct gtt gtc aaa aag atg aag gag acc tta aag gag aaa gct Asp Leu Ser Val Val Lys Lys Met Lys Glu Thr Leu Lys Glu Lys Ala 305 310 315 320			
aag ctc tgagctgagg aaacaaggtg tcctccatcc ccagtgccct cacatcttga Lys Leu			
ggatatgctt ctgtactttt taaaagctta tagttggat ggaaaacatt tttcttattt 1136 ttaagtgtta ttaatttatat ctatggaaaa actattcctg aaatatatac agtcttatgt 1196 cccaaaaaaaa aaa 1209			
<210> 11 <211> 322 <212> PRT <213> Homo sapiens			
<400> 11 Met Ser Leu Arg Pro Arg Arg Ala Cys Ala Gln Leu Leu Trp His Pro 1 5 10 15 Ala Ala Gly Met Ala Ser Trp Ala Lys Gly Arg Ser Tyr Leu Ala Pro 20 25 30			

Gly Leu Leu Gln Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly
 35 40 45
 Ile Gly Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val
 50 55 60
 Val Ile Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu
 65 70 75 80
 Leu Gln Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile
 85 90 95
 Gln Cys Asn Ile Arg Asn Glu Glu Val Asn Asn Leu Val Lys Ser
 100 105 110
 Thr Leu Asp Thr Phe Gly Lys Ile Asn Phe Leu Val Asn Asn Gly Gly
 115 120 125
 Gly Gln Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His
 130 135 140
 Ala Val Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala
 145 150 155 160
 Val Tyr Ser Ser Trp Met Lys Glu His Gly Ser Ile Val Asn Ile
 165 170 175
 Ile Val Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala
 180 185 190
 Ala Arg Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp
 195 200 205
 Ala Cys Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr
 210 215 220
 Ser Gln Thr Ala Val Glu Asn Tyr Gly Ser Trp Gly Gln Ser Phe Phe
 225 230 235 240
 Glu Gly Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu
 245 250 255
 Glu Val Ser Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe
 260 265 270
 Ile Thr Gly Gln Ser Val Asp Val Asp Gly Gly Arg Ser Leu Tyr Thr
 275 280 285
 His Ser Tyr Glu Val Pro Asp His Asp Asn Trp Pro Lys Gly Ala Gly
 290 295 300
 Asp Leu Ser Val Val Lys Lys Met Lys Glu Thr Leu Lys Glu Lys Ala
 305 310 315 320
 Lys Leu

<210> 12
 <211> 966
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(966)

<400> 12
 atg tcc ctg aga ccc aga agg gcc tgc gct cag ctg ctc tgg cac ccc 48
 Met Ser Leu Arg Pro Arg Arg Ala Cys Ala Gln Leu Leu Trp His Pro
 1 5 10 15
 gct gca ggg atg gcc tcc tgg gct aag ggc agg agc tac ctg gcg cct 96
 Ala Ala Gly Met Ala Ser Trp Ala Lys Gly Arg Ser Tyr Leu Ala Pro
 20 25 30
 ggt ttg ctg cag ggc caa gtg gcc atc gtc acc ggc ggg gcc acg ggc 144
 Gly Leu Leu Gln Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly
 35 40 45
 atc gga aaa gcc atc gtg aag gag ctc ctg gag ctg ggg agt aat gtg 192
 Ile Gly Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val

50	55	60	
gtc att gca tcc cgt aag ttg gag aga ttg aag tct gcg gca gat gaa Val Ile Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu 65 70 75 80			240
ctg cag gcc aac cta cct ccc aca aag cag gca cga gtc att ccc ata Leu Gln Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile 85 90 95			288
caa tgc aac atc cgg aat gag gag gag gtg aat aat ttg gtc aaa tct Gln Cys Asn Ile Arg Asn Glu Glu Glu Val Asn Asn Leu Val Lys Ser 100 105 110			336
acc tta gat act ttt ggt aag atc aat ttc ttg gtg aac aat gga gga Thr Leu Asp Thr Phe Gly Lys Ile Asn Phe Leu Val Asn Asn Gly Gly 115 120 125			384
ggc cag ttt ctt tcc cct gct gaa cac atc agt tct aag gga tgg cac Gly Gln Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His 130 135 140			432
gct gtg ctt gag acc aac ctg acg ggt acc ttc tac atg tgc aaa gca Ala Val Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala 145 150 155 160			480
gtt tac agc tcc tgg atg aaa gag cat gga gga tct atc gtc aat atc Val Tyr Ser Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile 165 170 175			528
att gtc cct act aaa gct gga ttt cca tta gct gtg cat tct gga gct Ile Val Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala 180 185 190			576
gca aga gca ggt gtt tac aac ctc acc aaa tct tta gct ttg gaa tgg Ala Arg Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp 195 200 205			624
gcc tgc agt gga ata cgg atc aat tgt gtt gcc cct gga gtt att tat Ala Cys Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr 210 215 220			672
tcc cag act gct gtg gag aac tat ggt tcc tgg gga caa agc ttc ttt Ser Gln Thr Ala Val Glu Asn Tyr Gly Ser Trp Gly Gln Ser Phe Phe 225 230 235 240			720
gaa ggg tct ttt cag aaa atc ccc gct aaa cga att ggt gtt cct gag Glu Gly Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile Gly Val Pro Glu 245 250 255			768
gag gtc tcc tct gtg gtc tgc ttc cta ctg tct cct gca gct tcc ttc Glu Val Ser Ser Val Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe 260 265 270			816
atc act gga cag tcg gtg gat gtg gat ggg ggc cgg agt ctc tat act Ile Thr Gly Gln Ser Val Asp Val Asp Gly Gly Arg Ser Leu Tyr Thr 275 280 285			864
cac tcg tat gag gta cca gat cat gac aac tgg ccc aag gga gca ggg His Ser Tyr Glu Val Pro Asp His Asp Asn Trp Pro Lys Gly Ala Gly 290 295 300			912
gac ctt tct gtt gtc aaa aag atg aag gag acc tta aag gag aaa gct Asp Leu Ser Val Val Lys Lys Met Lys Glu Thr Leu Lys Glu Lys Ala			960

305

310

315

320

aag ctc
Lys Leu

966

<210> 13
<211> 303
<212> PRT
<213> Rattus norvegicus

<400> 13
Met Gly Ser Trp Lys Ser Gly Gln Ser Tyr Leu Ala Ala Gly Leu Leu
1 5 10 15
Gln Asn Gln Val Ala Val Val Thr Gly Gly Ala Thr Gly Ile Gly Lys
20 25 30
Ala Ile Ser Arg Glu Leu Leu His Leu Gly Cys Asn Val Val Ile Ala
35 40 45
Ser Arg Lys Leu Asp Arg Leu Thr Ala Ala Val Asp Glu Leu Arg Ala
50 55 60
Ser Gln Pro Pro Ser Ser Thr Gln Val Thr Ala Ile Gln Cys Asn
65 70 75 80
Ile Arg Lys Glu Glu Val Asn Asn Leu Val Lys Ser Thr Leu Ala
85 90 95
Lys Tyr Gly Lys Ile Asn Phe Leu Val Asn Asn Ala Gly Gly Gln Phe
100 105 110
Met Ala Pro Ala Glu Asp Ile Thr Ala Lys Gly Trp Gln Ala Val Ile
115 120 125
Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala Val Tyr Asn
130 135 140
Ser Trp Met Lys Asp His Gly Gly Ser Ile Val Asn Ile Ile Val Leu
145 150 155 160
Leu Asn Asn Gly Phe Pro Thr Ala Ala His Ser Gly Ala Ala Arg Ala
165 170 175
Gly Val Tyr Asn Leu Thr Lys Thr Met Ala Leu Thr Trp Ala Ser Ser
180 185 190
Gly Val Arg Ile Asn Cys Val Ala Pro Gly Thr Ile Tyr Ser Gln Thr
195 200 205
Ala Val Asp Asn Tyr Gly Glu Leu Gly Gln Thr Met Phe Glu Met Ala
210 215 220
Phe Glu Asn Ile Pro Ala Lys Arg Val Gly Leu Pro Glu Glu Ile Ser
225 230 235 240
Pro Leu Val Cys Phe Leu Leu Ser Pro Ala Ala Ser Phe Ile Thr Gly
245 250 255
Gln Leu Ile Asn Val Asp Gly Gly Gln Ala Leu Tyr Thr Arg Asn Phe
260 265 270
Thr Ile Pro Asp His Asp Asn Trp Pro Val Gly Ala Gly Asp Ser Ser
275 280 285
Phe Ile Lys Lys Val Lys Glu Ser Leu Lys Lys Gln Ala Arg Leu
290 295 300

<210> 14
<211> 1108
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (102) ... (1034)

<400> 14
ggaatggatg ctgttggctt aaacctcccc ctgcctggg gtttgcaacc aggttctctg 60

caaaggccat cctttgtcat cccgctgtcc tgcagagcaa g atg ggg ctc atg gct	116		
Met Gly Leu Met Ala			
1	5		
gtc ctg atg cta ccc ctg ctg ctg gga atc agc ggc ctc ctc ttc	164		
Val Leu Met Leu Pro Leu Leu Leu Gly Ile Ser Gly Leu Leu Phe			
10	15	20	
att tac cag gag gca tcc agg ctg tgg tcg aag tct gcc gtg cag aac	212		
Ile Tyr Gln Glu Ala Ser Arg Leu Trp Ser Lys Ser Ala Val Gln Asn			
25	30	35	
aaa gtg gtg gtc atc aca gat gcc atc tca gga ctg gga aag gag tgt	260		
Lys Val Val Val Ile Thr Asp Ala Ile Ser Gly Leu Gly Lys Glu Cys			
40	45	50	
gct cgg gtg ttc cat gca ggt ggg gca agg ctg gtg ctg tgt gga aag	308		
Ala Arg Val Phe His Ala Gly Gly Ala Arg Leu Val Leu Cys Gly Lys			
55	60	65	
aac tgg gag gga ctg gag agc ctc tat gcc acc ttg acc agt gtg gct	356		
Asn Trp Glu Gly Leu Glu Ser Leu Tyr Ala Thr Leu Thr Ser Val Ala			
70	75	80	85
gac ccc agc aag aca ttc acc ccc aag ctg gtc ctc ctg gat ctc tca	404		
Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val Leu Leu Asp Leu Ser			
90	95	100	
gac att agc tgt gtt caa gat gtg gcc aaa gag gtc ctg gac tgc tac	452		
Asp Ile Ser Cys Val Gln Asp Val Ala Lys Glu Val Leu Asp Cys Tyr			
105	110	115	
ggc tgt gtg gac atc ctc atc aac aat gcc agc gtg aaa gtg aag ggg	500		
Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser Val Lys Val Lys Gly			
120	125	130	
cct gcc cac aag att tcc ctg gag ctt gac aaa aag atc atg gat gcc	548		
Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys Lys Ile Met Asp Ala			
135	140	145	
aac tac ttc gga ccc atc act tta acc aaa gtt ctg ctt ccc aac atg	596		
Asn Tyr Phe Gly Pro Ile Thr Leu Thr Lys Val Leu Leu Pro Asn Met			
150	155	160	165
atc tcc agg aga aca ggc cag att gtg tta gtg aac aac atc caa gcg	644		
Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val Asn Asn Ile Gln Ala			
170	175	180	
aag ttt gga atc ccg ttc cgc aca gct tat gca gcc tct aag cat gcc	692		
Lys Phe Gly Ile Pro Phe Arg Thr Ala Tyr Ala Ala Ser Lys His Ala			
185	190	195	
gtc atg ggc ttc ttt gac tgc ctc cga gcc gag gtt gag gaa tac gat	740		
Val Met Gly Phe Phe Asp Cys Leu Arg Ala Glu Val Glu Glu Tyr Asp			
200	205	210	
gtt gtg gtc agc acc gtg agc cca act ttc atc cgc tcc tac cgt gct	788		
Val Val Val Ser Thr Val Ser Pro Thr Phe Ile Arg Ser Tyr Arg Ala			
215	220	225	
tcc cct gag caa aga aac tgg gag aca tcc att tgt aaa ttc ttc tgc	836		
Ser Pro Glu Gln Arg Asn Trp Glu Thr Ser Ile Cys Lys Phe Phe Cys			
230	235	240	245

agg aag cta gcc tat ggc gtg cac ccg gtg gag gtg gct gag gaa gtg 884
 Arg Lys Leu Ala Tyr Gly Val His Pro Val Glu Val Ala Glu Glu Val
 250 255 260

atg cgc aca gta cggttggagg aag aac caa gag gtg ttc atg gcc aac ccg 932
 Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val Phe Met Ala Asn Pro
 265 270 275

gtt cct aag gct gcc gtg ttc atc cgc acc ttc ttc cct gag ttc ttc 980
 Val Pro Lys Ala Ala Val Phe Ile Arg Thr Phe Phe Pro Glu Phe Phe
 280 285 290

ttc gct gtg gtg gcc tgt ggg gtg aag gag aag ctc aat gtc cca gaa 1028
 Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys Leu Asn Val Pro Glu
 295 300 305

gag ggt taacctcggtg gccaaagggg tcactcaagg ggaataaagg ctttcctaga 1084
 Glu Gly
 310

gaaaaaaaaaaa aaaaaaaaaaaa aaaa 1108

<210> 15
 <211> 311
 <212> PRT
 <213> Mus musculus

<400> 15
 Met Gly Leu Met Ala Val Leu Met Leu Pro Leu Leu Leu Leu Gly Ile
 1 5 10 15
 Ser Gly Leu Leu Phe Ile Tyr Gln Glu Ala Ser Arg Leu Trp Ser Lys
 20 25 30
 Ser Ala Val Gln Asn Lys Val Val Ile Thr Asp Ala Ile Ser Gly
 35 40 45
 Leu Gly Lys Glu Cys Ala Arg Val Phe His Ala Gly Gly Ala Arg Leu
 50 55 60
 Val Leu Cys Gly Lys Asn Trp Glu Gly Leu Glu Ser Leu Tyr Ala Thr
 65 70 75 80
 Leu Thr Ser Val Ala Asp Pro Ser Lys Thr Phe Thr Pro Lys Leu Val
 85 90 95
 Leu Leu Asp Leu Ser Asp Ile Ser Cys Val Gln Asp Val Ala Lys Glu
 100 105 110
 Val Leu Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser
 115 120 125
 Val Lys Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys
 130 135 140
 Lys Ile Met Asp Ala Asn Tyr Phe Gly Pro Ile Thr Leu Thr Lys Val
 145 150 155 160
 Leu Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val
 165 170 175
 Asn Asn Ile Gln Ala Lys Phe Gly Ile Pro Phe Arg Thr Ala Tyr Ala
 180 185 190
 Ala Ser Lys His Ala Val Met Gly Phe Phe Asp Cys Leu Arg Ala Glu
 195 200 205
 Val Glu Glu Tyr Asp Val Val Ser Thr Val Ser Pro Thr Phe Ile
 210 215 220
 Arg Ser Tyr Arg Ala Ser Pro Glu Gln Arg Asn Trp Glu Thr Ser Ile
 225 230 235 240
 Cys Lys Phe Phe Cys Arg Lys Leu Ala Tyr Gly Val His Pro Val Glu
 245 250 255
 Val Ala Glu Glu Val Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val
 260 265 270
 Phe Met Ala Asn Pro Val Pro Lys Ala Ala Val Phe Ile Arg Thr Phe
 275 280 285

Phe	Pro	Glu	Phe	Phe	Ala	Val	Val	Ala	Cys	Gly	Val	Lys	Glu	Lys
290					295					300				
Leu	Asn	Val	Pro	Glu	Glu	Gly								
305					310									

<210> 16
<211> 933
<212> DNA
<213> Mus musculus

<220>
<221> CDS
<222> (1)...(933)

<400> 16																
atg	ggg	ctc	atg	gct	gtc	ctg	atg	cta	ccc	ctg	ctg	ctg	gga	atc	48	
Met	Gly	Leu	Met	Ala	Val	Leu	Met	Leu	Pro	Leu	Leu	Leu	Gly	Ile		
1			5				10						15			
agc	ggc	ctc	ctc	tcc	att	tac	cag	gag	gca	tcc	agg	ctg	tgg	tcg	aag	96
Ser	Gly	Leu	Leu	Phe	Ile	Tyr	Gln	Glu	Ala	Ser	Arg	Leu	Trp	Ser	Lys	
			20				25						30			
tct	gcc	gtg	cag	aaa	gtg	gtg	gtc	atc	aca	gat	gcc	atc	tca	gga	144	
Ser	Ala	Val	Gln	Asn	Lys	Val	Val	Val	Ile	Thr	Asp	Ala	Ile	Ser	Gly	
			35				40						45			
ctg	gga	aag	gag	tgt	gct	cgg	gtg	tcc	cat	gca	ggt	ggg	gca	agg	ctg	192
Leu	Gly	Lys	Glu	Cys	Ala	Arg	Val	Phe	His	Ala	Gly	Gly	Ala	Arg	Leu	
			50				55						60			
gtg	ctg	tgt	gga	aag	aac	tgg	gag	gga	ctg	gag	agc	ctc	tat	gcc	acc	240
Val	Leu	Cys	Gly	Lys	Asn	Trp	Glu	Gly	Leu	Glu	Ser	Leu	Tyr	Ala	Thr	
			65				70						75		80	
ttg	acc	agt	gtg	gct	gac	ccc	agc	aag	aca	tcc	acc	ccc	aag	ctg	gtc	288
Leu	Thr	Ser	Val	Ala	Asp	Pro	Ser	Lys	Thr	Phe	Thr	Pro	Lys	Leu	Val	
			85				90						95			
ctc	ctg	gat	ctc	tca	gac	att	agc	tgt	gtt	caa	gat	gtg	gcc	aaa	gag	336
Leu	Leu	Asp	Leu	Ser	Asp	Ile	Ser	Cys	Val	Gln	Asp	Val	Ala	Lys	Glu	
			100				105						110			
gtc	ctg	gac	tgc	tac	ggc	tgt	gtg	gac	atc	ctc	atc	aac	aat	gcc	agc	384
Val	Leu	Asp	Cys	Tyr	Gly	Cys	Val	Asp	Ile	Leu	Ile	Asn	Asn	Ala	Ser	
			115				120						125			
gtg	aaa	gtg	aag	ggg	cct	gcc	cac	aag	att	tcc	ctg	gag	ctt	gac	aaa	432
Val	Lys	Val	Lys	Gly	Pro	Ala	His	Lys	Ile	Ser	Leu	Glu	Leu	Asp	Lys	
			130				135						140			
aag	atc	atg	gat	gcc	aac	tac	tcc	gga	ccc	atc	act	tta	acc	aaa	gtt	480
Lys	Ile	Met	Asp	Ala	Asn	Tyr	Phe	Gly	Pro	Ile	Thr	Leu	Thr	Lys	Val	
			145				150						155		160	
ctg	ctt	ccc	aac	atg	atc	tcc	agg	aga	aca	ggc	cag	att	gtg	tta	gtg	528
Leu	Leu	Pro	Asn	Met	Ile	Ser	Arg	Arg	Thr	Gly	Gln	Ile	Val	Leu	Val	
			165				170						175			
aac	aac	atc	caa	gcg	aag	ttt	gga	atc	ccg	tcc	cgc	aca	gct	tat	gca	576
Asn	Asn	Ile	Gln	Ala	Lys	Phe	Gly	Ile	Pro	Phe	Arg	Thr	Ala	Tyr	Ala	
			180				185						190			

gcc tct aag cat gcc gtc atg ggc ttc ttt gac tgc ctc cga gcc gag	624
Ala Ser Lys His Ala Val Met Gly Phe Phe Asp Cys Leu Arg Ala Glu	
195 200 205	
gtt gag gaa tac gat gtt gtg gtc agc acc gtg agc cca act ttc atc	672
Val Glu Glu Tyr Asp Val Val Val Ser Thr Val Ser Pro Thr Phe Ile	
210 215 220	
cgc tcc tac cgt gct tcc cct gag caa aga aac tgg gag aca tcc att	720
Arg Ser Tyr Arg Ala Ser Pro Glu Gln Arg Asn Trp Glu Thr Ser Ile	
225 230 235 240	
tgt aaa ttc ttc tgc agg aag cta gcc tat ggc gtg cac ccg gtg gag	768
Cys Lys Phe Phe Cys Arg Lys Leu Ala Tyr Gly Val His Pro Val Glu	
245 250 255	
gtg gct gag gaa gtg atg cgc aca gta cgg agg aag aag caa gag gtg	816
Val Ala Glu Glu Val Met Arg Thr Val Arg Arg Lys Lys Gln Glu Val	
260 265 270	
ttc atg gcc aac ccg gtt cct aag gct gcc gtg ttc atc cgc acc ttc	864
Phe Met Ala Asn Pro Val Pro Lys Ala Ala Val Phe Ile Arg Thr Phe	
275 280 285	
ttc cct gag ttc ttc gct gtg gtg gcc tgt ggg gtg aag gag aag	912
Phe Pro Glu Phe Phe Ala Val Val Ala Cys Gly Val Lys Glu Lys	
290 295 300	
ctc aat gtc cca gaa gag ggt	933
Leu Asn Val Pro Glu Glu Gly	
305 310	

<210> 17
 <211> 491
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> aldehyde dehydrogenase domain

<400> 17
 Glu Trp Val Asp Ser Ala Ser Gly Lys Thr Phe Glu Val Val Asn Pro
 1 5 10 15
 Ala Asn Lys Gly Glu Val Ile Gly Arg Val Pro Glu Ala Thr Ala Glu
 20 25 30
 Asp Val Asp Ala Ala Val Lys Ala Ala Lys Glu Ala Phe Lys Ser Gly
 35 40 45
 Pro Trp Trp Ala Lys Val Pro Ala Ser Glu Arg Ala Arg Ile Leu Arg
 50 55 60
 Lys Leu Ala Asp Leu Ile Glu Glu Arg Glu Asp Glu Leu Ala Ala Leu
 65 70 75 80
 Glu Thr Leu Asp Leu Gly Lys Pro Leu Ala Glu Ala Lys Gly Asp Thr
 85 90 95
 Glu Val Gly Arg Ala Ile Asp Glu Ile Arg Tyr Tyr Ala Gly Trp Ala
 100 105 110
 Arg Lys Leu Met Gly Glu Arg Arg Val Ile Pro Ser Leu Ala Thr Asp
 115 120 125
 Gly Asp Glu Glu Leu Asn Tyr Thr Arg Arg Glu Pro Leu Gly Val Val
 130 135 140
 Gly Val Ile Ser Pro Trp Asn Phe Pro Leu Leu Ala Leu Trp Lys
 145 150 155 160
 Leu Ala Pro Ala Leu Ala Gly Asn Thr Val Val Leu Lys Pro Ser

165	170	175	
Glu Gln Thr Pro Leu Thr Ala Leu Leu Ala Glu Leu Ile Glu Glu			
180	185	190	
Ala Gly Ala Asn Asn Leu Pro Lys Gly Val Val Asn Val Val Pro Gly			
195	200	205	
Phe Gly Ala Glu Val Gly Gln Ala Leu Leu Ser His Pro Asp Ile Asp			
210	215	220	
Lys Ile Ser Phe Thr Gly Ser Thr Glu Val Gly Lys Leu Ile Met Glu			
225	230	235	240
Ala Ala Ala Ala Lys Asn Leu Lys Lys Val Thr Leu Glu Leu Gly Gly			
245	250	255	
Lys Ser Pro Val Ile Val Phe Asp Asp Ala Asp Leu Asp Lys Ala Val			
260	265	270	
Glu Arg Ile Val Phe Gly Ala Phe Gly Asn Ala Gly Gln Val Cys Ile			
275	280	285	
Ala Pro Ser Arg Leu Leu Val His Glu Ser Ile Tyr Asp Glu Phe Val			
290	295	300	
Glu Lys Leu Lys Glu Arg Val Lys Lys Leu Lys Leu Ile Gly Asp Pro			
305	310	315	320
Leu Asp Ser Asp Thr Asn Ile Tyr Gly Pro Leu Ile Ser Glu Gln Gln			
325	330	335	
Phe Asp Arg Val Leu Ser Tyr Ile Glu Asp Gly Lys Glu Glu Gly Ala			
340	345	350	
Lys Val Leu Cys Gly Gly Glu Arg Asp Glu Ser Lys Glu Tyr Leu Gly			
355	360	365	
Gly Gly Tyr Tyr Val Gln Pro Thr Ile Phe Thr Asp Val Thr Pro Asp			
370	375	380	
Met Lys Ile Met Lys Glu Glu Ile Phe Gly Pro Val Leu Pro Ile Ile			
385	390	395	400
Lys Phe Asp Leu Asp Glu Ala Ile Glu Leu Ala Asn Asp Thr Glu Tyr			
405	410	415	
Gly Leu Ala Ala Tyr Val Phe Thr Lys Asp Ile Leu Ala Arg Ala Phe			
420	425	430	
Arg Val Ala Lys Ala Leu Glu Ala Gly Ile Val Trp Val Asn Asp Val			
435	440	445	
Cys Val His Ala Ala Glu Pro Gln Leu Pro Phe Gly Gly Val His Gln			
450	455	460	
Ser Ser Gly Ile Gly Arg Glu His Gly Gly Lys Tyr Gly Leu Glu Glu			
465	470	475	480
Tyr Thr Glu Ile Lys Thr Val Thr Ile Arg Leu			
485	490		

<210> 18
<211> 671
<212> PRT
<213> Artificial Sequence

<220>
<223> aldehyde dehydrogenase oxidoreductase domain

<221> VARIANT
<222> 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108,
109, 110, 111, 112, 113, 114, 162, 163, 164, 165, 166, 167,
168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179,
180, 181, 182, 385, 386, 387, 388, 389, 390, 391
<223> Xaa = Any Amino Acid

<221> VARIANT
<222> 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403,
404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415,
416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427,
428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438

<223> Xaa = Any Amino Acid

<221> VARIANT

<222> 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529

<223> Xaa = Any Amino Acid

<400> 18

Arg	Ala	Gln	His	Leu	Thr	Arg	Leu	Ala	Glu	Val	Ile	Gln	Lys	His	Gln
1				5					10				15		
Arg	Leu	Leu	Trp	Thr	Leu	Glu	Ser	Leu	Val	Thr	Gly	Arg	Ala	Val	Arg
				20					25			30			
Glu	Val	Arg	Asp	Gly	Asp	Val	Gln	Leu	Ala	Gln	Gln	Leu	Leu	His	Tyr
				35				40			45				
His	Ala	Ile	Gln	Ala	Ser	Thr	Gln	Glu	Glu	Ala	Leu	Ala	Gly	Trp	Glu
				50				55			60				
Pro	Met	Gly	Val	Ile	Gly	Leu	Ile	Leu	Pro	Pro	Thr	Phe	Ser	Phe	Leu
	65				70				75			80			
Glu	Met	Met	Trp	Arg	Ile	Cys	Pro	Ala	Leu	Ala	Val	Gly	Val	Thr	Xaa
				85				90			95				
Xaa															
				100				105			110				
Xaa	Xaa	Gly	Glu	Leu	Gly	Pro	Phe	Pro	Gly	Ile	Leu	Asn	Val	Val	Ser
		115				120					125				
Gly	Pro	Ala	Ser	Leu	Val	Pro	Ile	Leu	Ala	Ser	Gln	Pro	Gly	Ile	Arg
	130				135				140						
Lys	Val	Ala	Phe	Cys	Gly	Ala	Pro	Glu	Glu	Gly	Arg	Ala	Leu	Arg	Arg
	145				150				155			160			
Ser	Xaa														
				165				170			175				
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Thr	Ala	Asp	Val	Asp	Ser	Ala	Val	Glu
				180				185			190				
Gly	Val	Val	Asp	Ala	Ala	Trp	Ser	Asp	Pro	Gly	Pro	Gly	Gly	Leu	Arg
	195					200			205						
Leu	Leu	Ile	Gln	Glu	Ser	Val	Trp	Asp	Glu	Ala	Met	Arg	Arg	Leu	Gln
	210					215				220					
Glu	Arg	Met	Gly	Arg	Leu	Arg	Ser	Gly	Arg	Gly	Leu	Asp	Gly	Ala	Val
	225				230				235			240			
Asp	Met	Gly	Ala	Arg	Gly	Ala	Ala	Ala	Cys	Asp	Leu	Val	Gln	Arg	Phe
				245				250			255				
Val	Arg	Glu	Ala	Gln	Ser	Gln	Gly	Ala	Gln	Val	Phe	Gln	Ala	Gly	Asp
		260				265				270					
Val	Pro	Ser	Glu	Arg	Pro	Phe	Tyr	Pro	Pro	Thr	Leu	Val	Ser	Asn	Leu
	275				280				285						
Pro	Pro	Ala	Ser	Pro	Cys	Ala	Gln	Val	Glu	Val	Pro	Trp	Pro	Val	Val
	290				295				300						
Val	Ala	Ser	Pro	Phe	Arg	Thr	Ala	Lys	Glu	Ala	Leu	Leu	Val	Ala	Asn
	305				310				315			320			
Gly	Thr	Pro	Arg	Gly	Gly	Ser	Ala	Ser	Val	Trp	Ser	Glu	Arg	Leu	Gly
				325				330			335				
Gln	Ala	Leu	Glu	Leu	Gly	Tyr	Gly	Leu	Gln	Val	Gly	Thr	Val	Trp	Ile
		340			345					350					
Asn	Ala	His	Gly	Leu	Arg	Asp	Pro	Ser	Val	Pro	Thr	Gly	Gly	Cys	Lys
		355			360					365					
Glu	Ser	Gly	Cys	Ser	Trp	His	Gly	Gly	Pro	Asp	Gly	Leu	Tyr	Glu	Tyr
	370				375				380						
Xaa															
	385				390				395			400			
Xaa															
		405				410				415					
Xaa															
	420				425					430					

<210> 19
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> short chain dehydrogenase domain

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<400> 19
Lys Val Ala Leu Val Thr Gly Ala Ser Ser Gly Ile Gly Leu Ala Ile
      5          10          15
Ala Lys Arg Leu Ala Lys Glu Gly Ala Lys Val Val Val Ala Asp Arg
      20          25          30
Asn Glu Glu Lys Leu Glu Lys Gly Ala Val Ala Lys Glu Leu Lys Glu
      35          40          45
Leu Gly Gly Asn Asp Lys Asp Arg Ala Leu Ala Ile Gln Leu Asp Val
      50          55          60
Thr Asp Glu Glu Ser Val Ala Ala Val Glu Gln Ala Val Glu Arg Leu
      65          70          75          80
Gly Arg Leu Asp Val Leu Val Asn Asn Ala Gly Gly Ile Ile Leu Leu
      85          90          95
Arg Pro Gly Pro Phe Ala Glu Leu Ser Arg Thr Met Glu Glu Asp Trp
      100         105         110
Asp Arg Val Ile Asp Val Asn Leu Thr Gly Val Phe Leu Leu Thr Arg
      115         120         125
Ala Val Leu Pro Leu Met Ala Met Lys Lys Arg Gly Gly Arg Ile
      130         135         140
Val Asn Ile Ser Ser Val Ala Gly Arg Lys Glu Gly Gly Leu Val Gly
      145         150         155         160
Val Pro Gly Gly Ser Ala Tyr Ser Ala Ser Lys Ala Ala Val Ile Gly
      165         170         175

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Leu Thr Arg Ser Leu Ala Leu Glu Leu Ala Pro His Gly Ile Arg Val
180 185 190
Asn Ala Val Ala Pro Gly Gly Val Asp Thr Asp
195 200

<210> 20
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> alpha2 macroglobulin family domain

<400> 20
Ile Asp Glu Asp Asp Ile Thr Ile Arg Ser Tyr Phe Pro Glu
1 5 10

<210> 21
<211> 127
<212> PRT
<213> Artificial Sequence

<220>
<223> oxidoreductase protein dehydrogenase

<400> 21
Asp Leu Ser Asp Ile Ser Cys Val Pro Asp Val Ala Lys Glu Val Leu
1 5 10 15
Asp Cys Tyr Gly Cys Val Asp Ile Leu Ile Asn Asn Ala Ser Val Lys
20 25 30
Val Lys Gly Pro Ala His Lys Ile Ser Leu Glu Leu Asp Lys Lys Ile
35 40 45
Met Asp Ala Asn Tyr Phe Gly Pro Ile Leu Thr Leu Thr Lys Ala Leu
50 55 60
Leu Pro Asn Met Ile Ser Arg Arg Thr Gly Gln Ile Val Leu Val Asn
65 70 75 80
Asn Ile Gln Gly Lys Phe Gly Ile Pro Phe Arg Thr Thr Tyr Ala Ala
85 90 95
Ser Lys His Ala Ala Ser Lys His Ala Ala Leu Gly Phe Phe Asp Cys
100 105 110
Leu Arg Ala Glu Val Glu Glu Tyr Asp Val Val Ile Ser Thr Val
115 120 125

<210> 22
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> S-adenosylmethionine synthetase domain

<400> 22
His Phe Gly Arg Glu Glu Val Asp Phe Pro Trp Glu
1 5 10

<210> 23
<211> 424
<212> PRT
<213> Artificial Sequence

<220>
<223> 3-beta hydroxysteroid dehydrogenase domain

<400> 23
Glu Leu Ser Glu Ser Leu Asp Met Ala Gly Leu Ser Cys Leu Val Thr
1 5 10 15
Gly Gly Gly Phe Leu Gly Arg His Ile Val Arg Glu Leu Leu Arg
20 25 30
Glu Gly Ser Leu Gln Glu Val Arg Val Phe Asp Leu Arg Phe Ser
35 40 45
Pro Glu Leu Asp Glu Asp Ser Ser Lys Leu Gln Val Ile Thr Lys Ile
50 55 60
Lys Tyr Ile Glu Gly Asp Val Thr Asp Lys Gln Asp Leu Ala Ala Ala
65 70 75 80
Leu Gln Gly Ile Ser Cys Cys Thr Leu Leu Asp Met Thr Leu Met Asp
85 90 95
Asp Val Val Ile His Thr Ala Ala Ile Ile Asp Val Phe Gly Glu Leu
100 105 110
Arg Val Ser Gly Ser Asp Leu Ser Phe Gly Val Thr Val Leu Phe Leu
115 120 125
Ala Val Thr Glu Gly Ser Tyr Val Val Phe Tyr Met Gly Ala Thr Asp
130 135 140
Leu Arg Lys Ala Ser Arg Asp Arg Ile Met Lys Val Asn Val Lys Gly
145 150 155 160
Thr Gln Asn Val Leu Asp Ala Cys Val Glu Ala Gly Val Arg Val Leu
165 170 175
Val Tyr Thr Ser Ser Met Glu Val Val Gly Pro Asn Ser Arg Gly Gln
180 185 190
Pro Ile Val Asn Gly Asp Glu Thr Thr Pro Tyr Glu Ser Thr Asp Asp
195 200 205
His Gln Asp Ala Tyr Pro Glu Ser Lys Ala Leu Ala Glu Lys Leu Val
210 215 220
Leu Lys Ala Asn Gly Ser Met Leu Lys Asn Gly Arg Leu Tyr Thr
225 230 235 240
Cys Ala Leu Arg Pro Ala Gly Ile Phe Glu Gly Asp Gln Phe Leu Val
245 250 255
Pro Phe Leu Arg Gln Leu Val Lys Asn Gly Leu Ala Lys Phe Arg Ile
260 265 270
Gly Asp Lys Asn Ala Leu Ser Asp Arg Val Tyr Val Gly Asn Val Ala
275 280 285
Trp Ala His Ile Leu Ala Ala Arg Ala Leu Gln Asp Pro Lys Lys Gly
290 295 300
Arg Glu Gly Ala Ser Ser Ile Ala Gly Gln Ala Tyr Phe Ile Ser Asp
305 310 315 320
Asp Ser Pro Val Asn Ser Tyr Asp Asp Phe Asn Arg Thr Leu Leu Lys
325 330 335
Ala Leu Gly Leu Arg Leu Pro Ser Thr Trp Arg Leu Pro Leu Pro Leu
340 345 350
Leu Tyr Val Leu Ala Tyr Leu Asn Glu Leu Leu Ser Trp Leu Leu Arg
355 360 365
Lys Leu Ala Leu Arg Tyr Thr Pro Leu Leu Asn Pro Tyr Thr Val Thr
370 375 380
Leu Ala Asn Thr Thr Phe Thr Phe Ser Thr Asn Lys Ala Lys Lys Asp
385 390 395 400
Leu Gly Tyr Glu Pro Leu Val Thr Trp Glu Glu Ala Arg Ala Lys Thr
405 410 415
Ile Glu Trp Ile Gln Glu Leu Glu

<210> 24
<211> 359
<212> PRT
<213> Artificial Sequence

<220>
<223> NAD dependent epimerase/dehydratase domain

<400> 24
Ile Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Arg
1 5 10 15
Glu Leu Leu Asn Asn Tyr Gly Asp Asp Lys Val Val Val Leu Asp Asn
20 25 30
Leu Thr Asp Tyr Tyr Gln Tyr Ala Gly Asn Glu Ala Arg Leu Glu Val
35 40 45
Val Glu Gly Asn Pro Arg Tyr Thr Phe Val Lys Gly Asp Ile Cys Asp
50 55 60
Arg Asp Leu Leu Asp Lys Val Phe Ala Glu His Gln Pro Asp Ala Val
65 70 75 80
Ile His Phe Ala Ala Glu Ser His Val Asp Arg Ser Ile Glu Lys Pro
85 90 95
Leu Ala Tyr Ile Asp Thr Asn Val Val Gly Thr Leu Thr Leu Leu Glu
100 105 110
Ala Ala Arg Asn Tyr Trp Ser Ala Leu Asp Glu Thr Lys Ala Gly Val
115 120 125
Lys Lys Phe Val Phe Ser Ser Thr Asp Glu Val Tyr Gly Asp Leu Glu
130 135 140
Ser Ile Pro Ile Ser Ala Phe Thr Glu Asp Thr Pro Tyr Asn Pro Ser
145 150 155 160
Ser Pro Tyr Gly Ala Ser Lys Ala Ser Ser Glu Leu Leu Val Arg Ala
165 170 175
Tyr His Arg Ala Tyr Gly Leu Pro Ala Ile Ile Leu Arg Tyr Phe Asn
180 185 190
Val Tyr Gly Pro Tyr Gln Ser Gly Arg Ile Gly Glu Asp Pro Asn Gly
195 200 205
Phe Pro Glu Lys Leu Ile Pro Leu Ile Ile Gln Asn Ala Leu Gly Lys
210 215 220
Gly Glu Pro Leu Pro Val Tyr Gly Asp Gly Tyr Pro Thr Pro Asp Gly
225 230 235 240
Thr Gln Val Arg Asp Trp Ile His Val Glu Asp His Ala Arg Ala Asn
245 250 255
His Leu Leu Ala Leu Thr Lys Gly Arg Ala Gly Lys Ser Glu Val
260 265 270
Tyr Asn Ile Gly Gly Asn Glu Tyr Ser Asn Leu Glu Val Val Glu
275 280 285
Ala Ile Glu Lys Leu Leu Gly Glu Leu Ala Pro Glu Lys Pro His Val
290 295 300
Lys Ala Lys Glu Asp Pro Ala Thr Phe Val Asp Asp Arg Pro Gly Asp
305 310 315 320
Asp Ala Arg Tyr Ala Ala Asp Ala Ser Lys Ile Lys Arg Glu Leu Gly
325 330 335
Trp Lys Pro Glu Val Thr Asn Leu Glu Glu Gly Leu Ala Asp Thr Val
340 345 350
Asn Trp Tyr Leu Glu Asn Glu
355

<210> 25
<211> 260

<212> PRT

<213> Artificial Sequence

<220>

<223> 3-beta hydroxysteroid dehydrogenase delta5 domain

<221> VARIANT

<222> 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150,
192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203,
204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215,
216, 217

<223> Xaa = Any Amino Acid

<400> 25

His Glu Val Asn Val Gln Gly Thr Arg Asn Val Ile Glu Ala Cys Val
1 5 10 15
Gln Thr Gly Thr Arg Phe Leu Val Tyr Thr Ser Ser Met Glu Val Val
20 25 30
Gly Pro Asn Thr Lys Gly His Pro Phe Tyr Arg Gly Asn Glu Asp Thr
35 40 45
Pro Tyr Glu Ala Val His Arg His Pro Tyr Pro Cys Ser Lys Ala Leu
50 55 60
Ala Glu Trp Leu Val Leu Glu Ala Asn Gly Arg Lys Val Arg Gly Gly
65 70 75 80
Leu Pro Leu Val Thr Cys Ala Leu Arg Pro Thr Gly Ile Tyr Gly Glu
85 90 95
Gly His Gln Ile Met Arg Asp Phe Tyr Arg Gln Gly Leu Arg Leu Gly
100 105 110
Gly Trp Leu Phe Arg Ala Ile Pro Ala Ser Val Glu His Gly Arg Val
115 120 125
Tyr Val Gly Asn Val Ala Trp Met His Val Xaa Xaa Xaa Xaa Xaa Xaa
130 135 140
Xaa Xaa Xaa Xaa Xaa Met Gly Gly Val Tyr Phe Cys Tyr Asp Gly
145 150 155 160
Ser Pro Tyr Arg Ser Tyr Glu Asp Phe Asn Met Glu Phe Leu Gly Pro
165 170 175
Cys Gly Leu Arg Leu Val Gly Ala Arg Pro Leu Leu Pro Tyr Trp Xaa
180 185 190
Xaa
195 200 205
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Pro Tyr Thr Leu Ala Val
210 215 220
Ala Asn Thr Thr Phe Thr Val Ser Thr Asp Lys Ala Gln Arg His Phe
225 230 235 240
Gly Tyr Glu Pro Leu Phe Ser Trp Glu Asp Ser Arg Thr Arg Thr Ile
245 250 255
Leu Trp Val Gln
260

<210> 26

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> 3-beta hydroxysteroid dehydrogenase delta5 domain

<400> 26

Val Tyr Leu Val Thr Gly Gly Cys Gly Phe Leu Gly Glu His Val Val

1	5	10	15
Arg	Met	Leu	Leu
Gln		Arg	Glu
20			

<210> 27
<211> 35
<212> PRT
<213> Artificial Sequence

<220>
<223> short chain dehydrogenase/reductase C2 domain

<400> 27
Gly Arg Leu Gly Glu Pro Glu Glu Ile Ala Asn Ala Val Val Phe Leu
1 5 10 15
Ala Ser Asp Ala Ala Ser Asp Ala Ala Ser Tyr Ile Thr Gly Gln Thr
20 25 30
Leu Val Val
35

<210> 28
<211> 181
<212> PRT
<213> Artificial Sequence

<220>
<223> oxidoreductase protein dehydrogenase NAD reductase domain

<400> 28
Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val Val Ile
1 5 10 15
Ala Lys Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu Leu Gln
20 25 30
Ala Asn Leu Pro Pro Thr Lys Gln Ala Arg Val Ile Pro Ile Gln Cys
35 40 45
Asn Ile Arg Asn Glu Glu Val Asn Asn Leu Val Lys Ser Thr Leu
50 55 60
Asp Thr Phe Gly Lys Ile Asn Phe Leu Cys Asn Asn Gly Gly Gln
65 70 75 80
Phe Leu Ser Pro Ala Glu His Ile Ser Ser Lys Gly Trp His Ala Val
85 90 95
Leu Glu Thr Asn Leu Thr Gly Thr Phe Tyr Met Cys Lys Ala Val Tyr
100 105 110
Ser Ser Trp Met Lys Glu His Gly Gly Ser Ile Val Asn Ile Ile Val
115 120 125
Pro Thr Lys Ala Gly Phe Pro Leu Ala Val His Ser Gly Ala Ala Arg
130 135 140
Ala Gly Val Tyr Asn Leu Thr Lys Ser Leu Ala Leu Glu Trp Ala Cys
145 150 155 160
Ser Gly Ile Arg Ile Asn Cys Val Ala Pro Gly Val Ile Tyr Ser Gln
165 170 175
Thr Ala Val Glu Asn
180

<210> 29
<211> 85

<212> PRT

<213> Artificial Sequence

<220>

<223> oxidoreductase protein dehydrogenase NAD reductase domain

<400> 29

Gly	Gln	Val	Ala	Ile	Val	Thr	Gly	Gly	Ala	Thr	Gly	Ile	Gly	Lys	Ala
1					5				10					15	
Ile	Val	Lys	Glu	Leu	Leu	Glu	Leu	Gly	Ser	Asn	Val	Val	Ile	Ala	Ser
					20				25					30	
Arg	Lys	Leu	Glu	Arg	Leu	Lys	Ser	Ala	Ala	Asp	Glu	Leu	Gln	Ala	Asn
					35				40				45		
Leu	Pro	Pro	Thr	Lys	Gln	Ala	Arg	Val	Ile	Pro	Ile	Gln	Cys	Asn	Ile
					50				55			60			
Arg	Asn	Glu	Glu	Glu	Val	Asn	Asn	Leu	Val	Lys	Ser	Thr	Leu	Asp	Thr
					65				70			75		80	
Phe	Gly	Lys	Ile	Asn											
					85										

<210> 30

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> oxidoreductase protein dehydrogenase NAD reductase domain

<400> 30

Ala	Leu	Glu	Trp	Ala	Cys	Ser	Gly	Ile	Arg	Ile	Asn	Cys	Val	Ala	Pro
1					5				10					15	
Gly	Val	Ile	Tyr	Ser	Gln	Thr									
					20										

<210> 31

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> glucose-1 dehydrogenase domain

<400> 31

Ser	Phe	Gln	Lys	Ile	Pro	Ala	Lys	Arg	Ile	Gly	Val	Pro	Glu	Glu	Val
1					5				10				15		
Ser	Ser	Val	Val	Cys	Phe	Leu	Leu	Ser	Pro	Ala	Ala	Ser	Phe	Ile	Thr
					20				25				30		
Gly	Gln	Ser	Cys	Asp	Cys	Asp	Gly	Gly	Arg	Ser	Leu	Tyr			
					35				40			45			

<210> 32

<211> 48

<212> PRT

<213> Artificial Sequence

<220>

<223> shikimate 5-dehydrogenase domain

<400> 32

Leu Gln Gly Gln Val Ala Ile Val Thr Gly Gly Ala Thr Gly Ile Gly
1 5 10 15
Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser Asn Val Val Ile
20 25 30
Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala Asp Glu Leu Gln
35 40 45

<210> 33

<211> 50

<212> PRT

<213> Artificial Sequence

<220>

<223> dehydrogenase domain

<400> 33

Gln Ser Phe Phe Glu Gly Ser Phe Gln Lys Ile Pro Ala Lys Arg Ile
1 5 10 15
Gly Val Pro Glu Glu Val Ser Ser Val Val Cys Phe Leu Leu Ser Pro
20 25 30
Ala Ala Ser Phe Ile Thr Gly Gln Ser Val Asp Val Asp Gly Gly Arg
35 40 45
Ser Leu
50

<210> 34

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> hypothetical protein domain

<400> 34

Tyr Leu Ala Pro Gly Gln Gly Gln Val Ala Ile Val Thr Gly Gly Ala
1 5 10 15
Thr Gly Ile Gly Lys Ala Ile Val Lys Glu Leu Leu Glu Leu Gly Ser
20 25 30
Asn Val Val Ile Ala Ser Arg Lys Leu Glu Arg Leu Lys Ser Ala Ala
35 40 45
Asp Glu Leu Gln
50